

**In the Specification:**

Please replace the paragraph beginning at line 14, page 5 with the following paragraph:

-- Figure 1, Panel A provides a sequence comparison showing the conservation of Oxa1p(-like) proteins in *B. subtilis*, *E. coli* and mitochondria of the yeast *S. cerevisiae*. In this Panel, the amino acid sequences of SpoIIIJ (SEQ ID NO:8) and YqjG (SEQ ID NO:9), and the partial sequences of YidC (SEQ ID NO:10) and Oxa1p (SEQ ID NO:11), comprising the conserved part as depicted in Panel B are shown. Identical residues are indicated in bold. The conserved transmembrane segments I-V (marked in gray shading) was predicted as described by Sipos and von Heijne (Sipos and von Heijne, Eur. J. Biochem., 213:1333-1340 [1993]). The putative SPase II cleavage sites (lipoboxes) in SpoIIIJ and YqjG are underlined. Notably, SpoIIIJ/YqjG orthologues with putative lipoprotein signal peptides have been found in several Gram-positive eubacteria (during the development of the present invention, SpoIIIJ/YQJG orthologues with putative lipoprotein signal peptides were identified in *B. anthracis*, *B. halodurans*, *B. stearothermophilus*, *Lactococcus lactis*, and *Staphylococcus aureus*). In this Panel, the numbers refer to the position of amino acids in the corresponding protein sequence. --